GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2003, 15:54:00 ; Search time 0.001 Seconds
(without alignments)
755.766 Million cell updates/sec

Title: us-09-831-455b-6
Perfect score: 1803
Sequence: 1 MSSWSRQRPKSPGGIQPHVS.....RCAGPEAVKGQTLLAVAKSQ 347

Scoring matrix: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 2 seqs, 1089 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=us-09-831-455b-6 -DB=a*.* -SUFFIX=pto
-OUT=align_6_nuc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1
-END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=4 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=4 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : a*.*:*
1: /home/sdavid/sdavid-tmp/sep03/steadman455/aa622495.gb_est1:*
2: /home/sdavid/sdavid-tmp/sep03/steadman455/aav87784.geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1107.8	61.4	686	2	AAV87784	EST clone ES35. H
c 2	165.4	9.2	686	2	AAV87784	EST clone ES35. H
3	116.4	6.5	403	1	AA622495	ACCESSION:AA622495
c 4	98.0002	5.4	403	1	AA622495	ACCESSION:AA622495

ALIGNMENTS

RESULT 1
AAV87784
ID AAV87784 standard; cDNA; 686 BP.
XX
AC AAV87784;
XX
DT 12-FEB-1999 (first entry)
XX
DE EST clone ES35.
XX
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO9845437-A2.
XX
PD 15-OCT-1998.
XX
PF 10-APR-1998; 98WO-US06956.
XX
PR 10-APR-1997; 97US-0837312.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1999-070078/06.
XX
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries
XX
PS Claim 1; Page 178; 641pp; English.
XX
CC The present sequence represents an expressed sequence tag (EST), and is
CC a polynucleotide of the invention. The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
CC therapy.
XX
SQ Sequence 686 BP; 137 A; 243 C; 177 G; 129 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	686
Score:	1107.80	Matches:	218
Percent Similarity:	98.64%	Conservative:	0
Best Local Similarity:	98.64%	Mismatches:	2
Query Match:	61.44%	Indels:	2
DB:	2	Gaps:	0

us-09-831-455b-6 (1-347) x AAV87784 (1-686)

```
Qy          1 MetSerSerTrpSerArgGlnArgProLysSerProGlyGlyIleGlnProHisValSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATGTCCTCTTGGAGCAGACAGCGACCAAAAAGCCCAGGGGGCATTCAACCCCATGTTTCT 86

Qy         21 ArgThrLeuPheLeuLeuLeuLeuAlaAlaSerAlaTrpGlyValThrLeuSerPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 AGAACTCTGTTCCTGCTGCTGCTGTTGGCAGCCTCAGCCTGGGGGGTCACCCTGAGCCCC 146

Qy         41 LysAspCysGlnValPheArgSerAspHisGlySerSerIleSerCysGlnProProAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAAGACTGCCAGGTGTTCCGCTCAGACCATGGCAGCTCCATCTCCTGTCAACCACCTGCC 206

Qy         61 GluIleProGlyTyrLeuProAlaAspThrValHisLeuAlaValGluPhePheAsnLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GAAATCCCCGGCTACCTGCCAGCCGACACCGTGCACCTGGCCGTGGAATTCTTCAACCTG 266

Qy         81 ThrHisLeuProAlaAsnLeuLeuGlnGlyAlaSerLysLeuGlnGluLeuHisLeuSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 ACCCACCTGCCAGCCAACCTCCTCCAGGGCGCCTCTAAGCTCCAAGAATTGCACCTCTCC 326
```

```
Qy        101 SerAsnGlyLeuGluSerLeuSerProGluPheLeuArgProValProGlnLeuArgVal 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 AGCAATGGGCTGGAAAGCCTCTCGCCCGAATTCCTGCGGCCAGTGCCGCAGCTGAGGGTG 386

Qy        121 LeuAspLeuThrArgAsnAlaLeuThrGlyLeuProProGlyLeuPheGlnAlaSerAla 140
              |||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db        387 CTGGATCTAACCCGAAACGCCCTGACCGGGCTGCCCTCGGGCCTCTTCCAGGCCTCAGCC 446

Qy        141 ThrLeuAspThrLeuValLeuLysGluAsnGlnLeuGluValLeuGluValSerTrpLeu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 ACCCTGGACACCCTGGTATTGAAAGAAAACCAGCTGGAGGTCCTGGAGGTCTCGTGGCTA 506

Qy        161 HisGlyLeuLysAlaLeuGlyHisLeuAspLeuSerGlyAsnArgLeuArgLysLeuPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 CACGGCCTGAAAGCTCTGGGGCATCTGGACCTGTCTGGGAACCGCCTCCGGAAACTGCCC 566

Qy        181 ProGlyLeuLeuAlaAsnPheThrLeuLeuArgThrLeuAspLeuGlyGluAsnGlnLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 CCCGGGCTGCTGGCCAACTTCACCCTCCTGCGCACCCTTGACCTTGGGGAGAACCAGTTG 626

Qy        201 GluThrLeuProProAspLeuLeuArgGlyProLeuGlnLeuGluArgLeuHis-LeuGl 220
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||
Db        627 GAGACCTTGCCACCTGACCTCCTGAGGGGTCCGCTGCAATTAGAACGGCA-CATTCTCGA 685

Qy        220 u 220
              |
Db        686 G 686

RESULT 2
AAV87784/c
ID   AAV87784 standard; cDNA; 686 BP.
XX
AC   AAV87784;
XX
DT   12-FEB-1999  (first entry)
XX
DE   EST clone ES35.
XX
KW   Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW   tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW   chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW   receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS   Homo sapiens.
XX
PN   WO9845437-A2.
XX
PD   15-OCT-1998.
XX
PF   10-APR-1998;   98WO-US06956.
XX
PR   10-APR-1997;   97US-0837312.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1999-070078/06.
XX
PT   New polynucleotides encoding human secreted proteins - derived from
PT   e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT   ovary, pituitary, retina and colon cDNA libraries
XX
PS   Claim 1; Page 178; 641pp; English.
XX
CC   The present sequence represents an expressed sequence tag (EST), and is
CC   a polynucleotide of the invention. The polynucleotides of the invention
CC   are all secreted EST sequences isolated from a variety of human tissue
CC   sources. The EST sequences and proteins encoded by them are predicted to
CC   have useful biological activities which would make them suitable for
CC   treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The EST sequences are also stated to be useful for gene
CC   therapy.
XX
SQ   Sequence 686 BP; 137 A; 243 C; 177 G; 129 T; 0 other;

Alignment Scores:
Pred. No.:              0           Length:          686
Score:                  165.40      Matches:         88
Percent Similarity:     23.71%      Conservative:    22
Best Local Similarity:  18.97%      Mismatches:      62
Query Match:            9.17%       Indels:          301
DB:                     2           Gaps:            6

us-09-855-455b-6 (1-347) x AAV87784 (1-686)

Qy         27 LeuLeuLeuAlaAlaSerAlaTrpGlyValThrLeuSerProLysAspCysGlnValPhe 46
              :::|||:::||||||                    |||       ||||||
Db        672 GTTCTAATTGCAGCG--------------------GACCCCTCAGGAGGTCAGGTGGCA 634

Qy         47 ArgSerAspHisGlySer-------SerIleSerCys---------------------- 56
              ||||||     ||||||       |||     |||
Db        633 AGGTCTCCAACTGGTTCTCCCCAAGGTCAA--GGGTGCGCAGGAGGGTGAAGTTGGCCAG 576

Qy         57 GlnProProAlaGluIleProGlyTyrLeuProAlaAspThrValHisLeuAlaValGlu 76
              ||||||      :::   |||  :::|||   |||   |||     |||   |||
Db        575 CAGCCCGGGGGGCAGTTTCCGGAGGCGGTTCCCA--GACAG-GTCCAGAT-GCCCCAGAG 520

Qy         77 PhePheAsnLeuThrHisLeuProAlaAsnLeuLeuGlnGly------AlaSerLys-Le 94
                                              |||   |||      |||:::::: ||
Db        519 -------------------------------CTTTCAGGCCGTGTAGCCACGAGACCT 493

Qy         94 uGlnGluLeuHisLeu----SerSerAsn----------------------GlyLeuGl 105
              ||||:::|||   |||   |||  |||                       ||||||||
Db        492 CCAGGACCTCCAGCTGGTTTTCTTTCAATACCAGGGTGTCCAGGGTGGCTGAGGCCTGGA 433

Qy        105 uSerLeu-------SerPro-------GluPhe---LeuArgProVal-ProGlnLeuAr 119
              |             ||||||       |||   |||   |||    ||||||||||
Db        432 AGAGGCCCGAGGGCAGCCCGGTCAGGGCGTTTCGGGTTAGATCCAGCACCCTCAGCTGCG 373

Qy        119 gValLeuAspLeuThrArgAsnAlaLeuThrGlyLeuProProGlyLeuPheGlnAlaSe 139
              |
Db        372 G---------------------------------------------------------- 372

Qy        139 rAlaThrLeuAspThrLeuValLeuLysGluAsnGlnLeuGluValLeuGluValSerTr 159
                                                                      ||
Db        371 ----------------------------------------------------------CACTG 367

Qy        159 pLeuHisGlyLeuLysAlaLeuGlyHisLeuAspLeuSerGlyAsnArgLeuArgLysLe 179
              |   |||::::::|||
Db        366 GCC-GCAGGAATTCGGGCG---------------------------------------- 349

Qy        179 uProProGlyLeuLeuAlaAsnPheThrLeuLeuArgThrLeuAspLeuGlyGluAsnGl 199

Db        349 ---------------------------------------------------------- 349

Qy        199 nLeuGluThrLeuProProAspLeuLeuArgGly-------ProLeuGlnLeuGluArg- 216
                                                |||||     |||:::   |||||||||
Db        348 ----------------------------AGAGGCTTTCCAGCCCATTG--CTGGAGAGGT 319

Qy        217 -------LeuHisLeuGluGly-------AsnLysLeu-----GlnValLeuGlyLysAs 230
                    |||   |||   |||          :::|||     ||||||
Db        318 GCAATTCTTGGAGCTTAGAGGCGCCCTGGAGGAGGTTGGCTGGCAGGTG---------- 270

Qy        230 pLeuLeuLeuProGlnProAspLeuArgTyrLeuPheLeuAsnGly----------AsnL 247
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Db        269 ----------------------------------------GGTCAGGTTGAAGAATT 253
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Qy        247 ysLeuAlaArg------ValAlaAlaGly-AlaPheGlnGlyLeuArgGln---LeuAsp 263
              ||||||      |||:::|||||| |   :::||| ||||||  :::|||
Db        252 CCACGGCCAGGTGCACGGTGTCGGCTGGCAGGTAGCCGGGGATTTCGGCAGGTGGTTGAC 193

Qy        264 MetLeuAspLeuSerAsnAsnSerLeuAlaSerValProGluGlyLeuTrpAlaSerLeu 283
              |||  |||  :::  |||:::      |||      ||||||  |||
Db        192 AGGA--GATGG-AGCTGCCATGGTCTGAGCGGAACACCTGGCAGTCTTTGGGGCTCAG-- 138

Qy        284 GlyGlnPro----------AsnTrpAspMetArgAsp-GlyPhe----AspIle 296
              |||  |||           |||         |||:::   |||   ::::::
Db        137 GGTGACCCCCCAGGCTGAGGCTGCCAACAGCAGCAGCAGGAACAGAGTTCTAGAAACATG 78

Qy        297 SerGlyAsn---ProTrpIleCysAspGlnAsnLeuSerAspLeuTyrArgTrp---Leu 314
              |||   ||||||                                  |||   |||
Db         77 GGGTTGAATGCCCCCTGGGCTTTT----------------------TGGTCGCTG 45

Qy        315 GlnAla-GlnLysAspLys---------MetPheSerGln 324
              ||| |||:::|||       :::|||  :::
Db         44 CCTGCTCCAAGAGGACATGGTAGTAGGCCTCTTTGGCCGA 5
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RESULT 3
AA622495
LOCUS AA622495 403 bp mRNA linear EST 14-OCT-1997
DEFINITION nq59b04.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148143 3' similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION AA622495
VERSION AA622495.1 GI:2526371
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 403)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1148143"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Co9"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4). "

BASE COUNT 105 a 89 c 117 g 92 t

Alignment Scores:

Pred. No.:	0	Length:	403
Score:	116.40	Matches:	45
Percent Similarity:	20.69%	Conservative:	21
Best Local Similarity:	14.11%	Mismatches:	29

Query Match: 6.46% Indels: 225
DB: 1 Gaps: 6

us-09-831-455b-6 (1-347) x AA622495 (1-403)

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Qy        134 GlyLeuPheGlnAlaSerAlaThrLeuAspThrLeuValLeuLysGluAsnGlnLeuGlu 153
              |||||||||
Db         13 GGGTTATTT---------------------------------------------------- 21

Qy        154 ValLeuGluValSerTrpLeuHisGlyLeuLysAlaLeuGlyHisLeu-----AspLeuS 172
                                       :::|||  ||||||  |||       ||||
Db         22 --------------------------ATTAAACCCCTTGGTT--CTGACCCCAAGCTAA 52

Qy        172 erGlyAsnArgLeuArgLysLeu----------ProProGlyLeuLeuAlaAsnPheTh 188
              |||||   :::   :::   |||          ||||||
Db         53 GTGGGACTCAGCATCAGACCCTGCACTCAGAGAGCCCCCT------------------- 92

Qy        188 rLeuLeuArgThrLeuAspLeuGlyGluAsnGlnLeuGluThrLeuProProAspLeuLe 208
                          ||||||||||:::   :::   |||
Db         93 ---------------GACTTGGGGAAGACAGAGTCAGAG------------------- 116

Qy        209 uArgGlyProLeuGlnLeuGluArgLeuHisGluGluGly--AsnLysLeuGlnValLeu 227
              :::|||        :::   |||      |||||||||  :::|||
Db        117 -AAAGGCAGCCCCAGTGTGGCCAGGGCTCAGCTGGAAGGAAGGACAAG------------ 163

Qy        228 GlyLysAspLeuLeuLeuProGlnProAspLeuArgTyrLeuPheLeuAsnGlyAsnLys 247

Db        163 ---------------------------------------------------------- 163

Qy        248 LeuAlaArgValAlaAlaGlyAlaPheGlnGlyLeuArgGlnLeuAspMetLeuAspLeu 267

Db        163 ---------------------------------------------------------- 163

Qy        268 SerAsnAsnSerLeuAlaSerValProGluGlyLeuTrpAlaSerLeuGlyGlnProAsn 287
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Db        164 ------------------------------------------GGGCTGGGAGAACCCAGA 181

Qy        288 ------------TrpAspMetArgAspGly-PheAspIleSerGlyAsnProTrp----- 301
                          |||:::      :::||| |||          |||   ||||||
Db        182 GTTCAAGAGATCTGGGAAACAGGGAACGGCATTCCAGACGGAGGGCACACCTTGGGCATG 241

Qy        302 ----------------IleCysAspGlnAsnLeuSerAspLeuTyrArgTrpLeuGln- 315
                              :::|||   :::                :::   |||::::::
Db        242 GGTAAGGAAAGCCCATCGTGTGTTCTAGGAAG-----------CATGGATGGATGAAAC 289

Qy        316 ---------AlaGlnLysAspLysMetPheSerGlnAsnAspThrArgCysAlaGlyPro 332
                      |||      |||                                    |||
Db        290 GGGGTCCCAGCCGCTATGGAC---------------------------------AGCCCC 316

Qy        333 Glu-----AlaValLysGly-----------------------------------Gln 338
              |||     |||||||||                                     :::
Db        317 GAGTTTCACCTGTAAAAGGCAGGATTATTTGTTTTTAATTTTAATTTTAATTTTTTTGAG 376

Qy        339 ThrLeuLeu-AlaValAlaLysSer 346
              |||:::||| :::|||||:::::
Db        377 ACAGTCTTGCTCTGTCGCCCAGGCT 401
```

RESULT 4
AA622495/c
LOCUS AA622495 403 bp mRNA linear EST 14-OCT-1997
DEFINITION nq59b04.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148143 3' similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION AA622495
VERSION AA622495.1 GI:2526371
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 403)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

```
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
            , Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .403
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1148143"
                     /tissue_type="colon tumor RER+"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Co9"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     RER+ colon tumor, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is not normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                     ). "
BASE COUNT      105 a     89 c    117 g     92 t

Alignment Scores:
Pred. No.:              0             Length:         403
Score:                  98.00         Matches:        53
Percent Similarity:     24.52%        Conservative:   11
Best Local Similarity:  20.31%        Mismatches:     41
Query Match:            5.44%         Indels:         158
DB:                     1             Gaps:           4

us-09-831-455b-6 (1-347) x AA622495 (1-403)

Qy          84 ProAlaAsnLeuLeuGlnGlyAlaSerLysLeuGlnGluLeuHisLeuSerSerAsn--- 102
               |||           :::      ||||||      :::|||   |||   :::|||
Db         399 CCTGGGCGACAGAGCAAGACTGTCTCAAAAAAATTAAAATTAAAATTAAAAACAAATAAT 340

Qy         103 ----------------------GlyLeuGlu----SerLeuSerProGluPheLeuAr 113
                                    ||||||        |||   |||   |||:::
Db         339 CCTGCCTTTTACAGGTGAAACTCGGGGCTGTCCATAGCGGCTGGGACCCCGTTTCATCCA 280

Qy         113 gPro--ValProGln--LeuArgValLeuAspLeuThr--------ArgAsnAlaLeu-- 128
                |||  :::|||:::     |||        ||||||        |||   ||||||
Db         279 TCCATGCTTCCTAGAACACACGATGGGCTTTCCTTACCCATGCCCAAGGTGTGCCCTCCG 220

Qy         129 ThrGlyLeuProProGlyLeuPhe--GlnAlaSerAlaThrLeuAspThrLeuValLeuL 148
               :::|||:::|||      ||||||  |||   |||   ||||||   :::
Db         219 TCTGGAATGCCGT--TCCCTGTTTCCCAGATCTCTTGAACTCTGGGTTCT---------- 172

Qy         148 ysGluAsnGlnLeuGluValLeuGluValSerTrpLeuHisGlyLeuLysAlaLeuGlyH 168

Db         172 ---------------------------------------------------------- 172

Qy         168 isLeuAspLeuSerGlyAsnArgLeuArgLysLeuProProGlyLeuLeuAla-AsnPhe 187
                                                  |||      |||.:: :::|||
Db         171 ------------------------------------ --CCCAGCCCTTGTCCTTCCTTC 150

Qy         188 ThrLeu---LeuArgThrLeuAspLeuGlyGluAsnGlnLeuGluThrLeuProPro- 205
                |||    |||  ||||||  |||                              |||
Db         149 CAGCTGAGCCCTGGCCACACTGGGGCTG----------------------------CCTTT 117

Qy         206 ----AspLeuLeuArgGlyProLeuGlnLeuGluArgLeuHisLeuGluGlyAsnLysLe 224
                    |||  |||    |||  |||
Db         116 CTGTGACT--CTGTCTTCCCCAAGTCAG------------------------------- 91

Qy         224 uGlnValLeuGlyLysAspLeuLeuLeuProGlnProAspLeuArgTyrLeuPheLeuAs 244

Db          91 ---------------------------------------------------------- 91

Qy         244 nGlyAsnLysLeuAlaArgValAlaAlaGlyAlaPhe------GlnGlyLeuArgGlnLe 262
                                                 ||||||      |||||||||
Db          90 --------------------------GGGGCTCTCTGAGTGCAGGGTCTGATG----- 64

Qy         262 uAspMetLeuAspLeuSerAsnAsn-SerLeuAlaSerValProGluGlyLeu 279
                               ||||||      ||||||   |||   |||   ||||||
Db          63 ------------CTGAGTCCCACTTAGCTTGGGGTCAGAACCAAGGGGTTTA 24


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GenCore version 5.1.6

OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 331 residues

Total number of hits satisfying chosen parameters: 1

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : baa31994.genpept:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
BAA31994

Query Match 24.1%; Score 434.5; DB 1; Length 331;
Best Local Similarity 36.0%; Pred. No. 0;
Matches 107; Conservative 46; Mismatches 129; Indels 15; Gaps 4;

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     251  LDLSDNELTT MEPPVYKTSA NLSLDLSGNP WACDCRLDNL LTWVNEHNIH

     301  LYSKEEIVCA SPKHFKGECA TSLHKSQICP C
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Inhibition of phospholipase A_2

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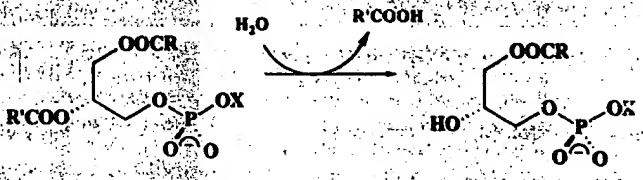
ABSTRACT **Phospholipases A_2 are involved in inflammatory processes such as the liberation of free arachidonic acid from the membrane pool for the biosynthesis of eicosanoids. Inhibitors of these enzymes are proving useful in determining the biological roles of phospholipases A_2 in complex cellular processes and may also have therapeutic potential. Inhibition of these lipolytic enzymes is more difficult to characterize as the enzymatic reaction occurs at a lipid/water interface. This review focuses on the description of a number of classes of rationally designed phospholipase A_2 inhibitors. The development of a theoretical framework for the proper analysis of inhibitors is presented. Structural studies of phospholipase A_2-inhibitor complexes suggest how the lipolysis reaction is catalyzed. Finally, some recent results on the use of phospholipase A_2 inhibitors in living cells and tissues are revealed.—Gelb, M. H., Jain, M. K., Berg, O. G. Inhibition of phospholipase A_2. *FASEB J.* 8: 916-924; 1994.**

Key Words: lipases • inhibitors • arachidonic acid • eicosanoids • protein-lipid interactions

PHOSPHOLIPASES A_2 (PLA_2s)[2] CATALYZE THE hydrolysis of the ester linkage at the *sn*-2 position of phospholipids to produce free fatty acids and lysophospholipids (Scheme I) (1).



Scheme I

The secreted enzymes ($sPLA_2$s) from pancreas (2), venoms (3), and inflammatory cells and exudates (4, 5) are the best characterized. These enzymes are small (molecular mass near 14 kDa), require millimolar amounts of Ca^{2+} as a catalytic cofactor but not for binding of the enzyme to membranes (6), and are related both in terms of primary (7) and three-dimensional structure (8–15). The $sPLA_2$s display almost no preference for different types of naturally occurring phospholipid head groups (substituent X in Scheme I) or the structure of the fatty acyl chains attached to the glycerol backbone (16).

Recently, a high molecular mass (87 kDa) cytosolic phospholipase A_2 ($cPLA_2$) has been found in human, bovine, and rabbit platelets (17–19), rodent macrophage cell lines (20, 21, 22), human monocytic cell lines (U937 and THP1) (23–26), and rat kidney (27). In contrast to the $sPLA_2$s, these $cPLA_2$s are activated by submicromolar amounts of Ca^{2+} and preferentially hydrolyze phospholipids that have arachidonic acid at the *sn*-2 position. The $cPLA_2$ is found in the cytosol of cells in the absence of Ca^{2+}, and it translocates to the particulate fraction in the presence of submicromolar amounts of Ca^{2+} (23, 24, 26–30). Calcium also promotes the binding of the enzyme to phospholipid vesicles in vitro (31, 32). Isolation of the cDNA encoding the $cPLA_2$ from U937 cells indicates that the enzyme has no regions that are homologous to the sequences of $sPLA_2$s (23, 33). Furthermore, the amino acid sequence reveals a stretch of 45 residues in the amino-terminal region that shows homology to Ca^{2+}-dependent forms of protein kinase C and other Ca^{2+}-dependent membrane binding proteins. A 140 amino acid fragment of this enzyme that contains the amino terminus was shown to bind to membranes in the presence of submicromolar amounts of Ca^{2+} (23).

Gross (34) and co-workers have identified a novel Ca^{2+}-independent PLA_2 found in myocardial cytosol. This enzyme prefers plasmalogens that contain arachidonic acid at the *sn*-2 position. Bovine brain cytosol also contains Ca^{2+}-independent PLA_2 (35).

Undoubtedly other PLA_2s in cells are involved in phospholipid remodeling and catabolism and in the degradation of phospholipids with oxidatively damaged fatty acyl chains (36).

The $sPLA_2$ found in inflammatory cells and exudates is almost certainly involved in inflammatory processes (see, for example, refs 37–42). This enzyme is often called the nonpancreatic secreted $sPLA_2$ because its amino acid sequence is more closely related to those of the $sPLA_2$s in the venoms from crotalids and viperids (type II enzymes) rather than to those from pancreas (type I enzymes) (7). This enzyme is secreted from activated platelets, mast cells, and other cell types in response to agonists. The role of this enzyme in the degradation of foreign bacteria appears certain (39), its role in mast cell histamine release and T cell activation is being clarified (43, 44), and its involvement in liberating arachidonic acid from the membrane in, for example, a macrophage-derived cell line and endothelial cells has recently been suggested (45, 46). Because arachidonate metabolites are potent mediators of allergic and inflammatory reactions, PLA_2 inhibitors are expected to have therapeutic value. The pancreatic $sPLA_2$, also called a type I $sPLA_2$, is found in tissues other than those of digestive function and appears to have a proinflammatory role (47). This enzyme is thought to bind to cells via a specific receptor lead-

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[2]Abbreviations: PLA_2, phospholipase A_2; $cPLA_2$, 87-kDa calcium-dependent cytosolic PLA_2 found in mammalian cells; $sPLA_2$, 14-kDa secreted calcium-dependent PLA_2 found in venoms, digestive fluids, and mammalian inflammatory exudates and cells.

0892-6638/94/0008-0916/$01.50.

ing to the induction of cyclooxygenase and the subsequent rise in levels of prostaglandins. Evidence is mounting to suggest that the cPLA$_2$ functions in a signal-transduction pathway leading to the rapid release of arachidonic acid from membranes for the biosynthesis of eicosanoids (48–50). The Ca^{2+}-independent PLA$_2$ may be involved in the degradation of membranes that accompanies myocardial infarction (34) and in the liberation of free arachidonate in hormone-stimulated aortic smooth muscle cells (51). For all of these reasons, most major pharmaceutical companies have ongoing programs aimed at discovering new inhibitors of PLA$_2$s.

The analysis of PLA$_2$ inhibition is more difficult than for most enzymes because the enzymatic hydrolysis of naturally occurring, long-chain phospholipids necessarily occurs at the lipid/water interface. The present article focuses on the design and analysis of tight-binding inhibitors of PLA$_2$s that have been carried out in the authors' laboratories. The rationale for the design of the inhibitors is discussed because it relates to the catalytic mechanism of PLA$_2$; this is revealed by X-ray diffraction analysis of PLA$_2$-inhibitor complexes. The problem of defining the mode of action of inhibitors of interfacial catalysis by PLA$_2$s is also discussed, as is the development of experimental techniques for analyzing the inhibition. Finally, initial results of PLA$_2$ inhibition studies with living cells and organs are discussed as they bear on the biological functions of PLA$_2$s.

INTERFACIAL CATALYSIS BY PLA$_2$: THE KINETIC PARADIGM

Before discussing PLA$_2$ inhibition, it is necessary to briefly describe some basic features of interfacial catalysis by this enzyme. As naturally occurring phospholipids are essentially insoluble in water and thus form aggregates, PLA$_2$s must be able to bind to such aggregates in order to gain access to substrate. Two modes of interfacial catalysis can be envisioned, and are illustrated in **Fig. 1.** In mode 1, it is imagined that the enzyme has a surface that can anchor it to a phospholipid aggregate such as a bilayer and that the enzyme also contains a topologically distinct active site where the lipolysis reaction takes place. In this mode, the enzyme is able to bind to the bilayer without a phospholipid molecule bound in its active site; the active site binding occurs after the enzyme binds to the interface. Thus, the following enzyme species occur in mode 1: E is the enzyme in the aqueous phase, E* is the enzyme bound to the interface but with its active site devoid of substrate and filled with solvent, E*S is the enzyme bound to the interface and with its active site occupied by a single substrate molecule (E*S is analogous to the well-known Michaelis complex, ES, for an enzyme operating in a homogeneous, aqueous-phase environment), and E*P is the enzyme bound to the interface with lipolysis products (fatty acid and lysophospholipid) in its active site. Interfacial catalysis may not necessarily proceed according to mode 1. As shown in Fig. 1, mode 2 can be imagined in which the binding of the enzyme to the interface and the loading of its active site with a molecule of substrate are the same step. In this case, the enzyme species E* does not exist.

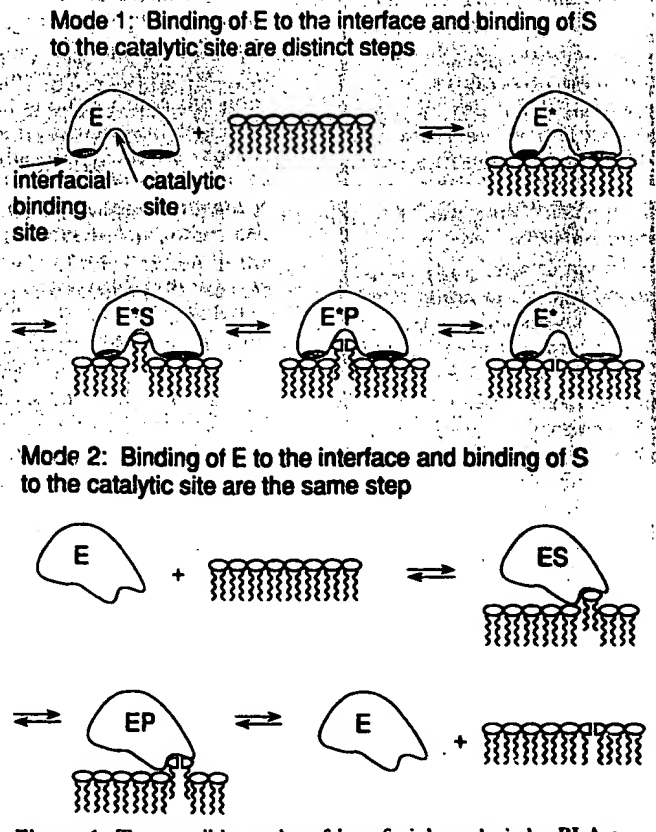


Figure 1. Two possible modes of interfacial catalysis by PLA$_2$s.

As will become clear throughout this review, the distinction between these modes is critical for a proper understanding of most aspects of interfacial catalysis including inhibition. The distinction between these modes comes from considering the possibility of processive interfacial catalysis. In the present context, processivity means that the enzyme can remain bound to a phospholipid vesicle during the course of more than one lipolysis turnover cycle. The most extreme type of processivity is when the enzyme hydrolyzes all the substrate in the outer layer of a phospholipid vesicle without ever leaving the surface. This has been called interfacial catalysis in the scooting mode (52) and is schematically illustrated in **Fig. 2.** Scooting mode catalysis has been observed for sPLA$_2$s from a variety of sources (venoms, pancreatic juices, and human synovial fluid; 52–54) and for the cPLA$_2$ from human U937 cells (55). The fact that processive catalysis occurs rules out mode 2 from further consideration. This is because in mode 2, the enzyme necessarily lets go of the interface when the lipolysis products are released from the active site, and the enzyme has no "memory" to enable it to return to the same phospholipid vesicle from which it was previously bound. On the other hand, in mode 1 catalysis the binding of the enzyme to the interface (E→E*) is independent of the binding of substrate in the active site (E* + S→E*S). If the E to E* step is sufficiently favorable so that the residency time of the enzyme on the interface is longer than the time it takes to complete a lipolysis reaction, processive catalysis will occur. Spectroscopic and chromatographic techniques have shown that sPLA$_2$s bind to phospholipid vesicles and phospholipid-containing detergent micelles (2, 56–58), but the fact that this binding is independent of the binding of a substrate molecule to the active site comes only from the demonstration that the reaction can be processive (52). Also, pig pancreatic sPLA$_2$, containing an active site-directed alkylating agent (*p*-bromo-phenacyl group attached to the catalytic histidine residue), is still able to bind to phospholipid aggregates even though substrate cannot bind to the active site because of steric clash with the inactivator (59). To the extent that this property of the inactivated enzyme applies to the native enzyme, this result is further evidence for the mode 1 nature of PLA$_2$-catalyzed reactions.

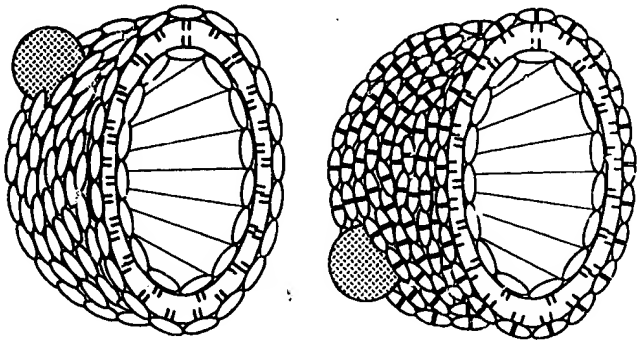


Figure 2. Schematic illustration of the PLA_2-catalyzed hydrolysis of vesicles in the highly processive scooting mode. The enzyme (small sphere) remains irreversibly bound to the vesicle, and only the phospholipids in the outer leaflet of the bilayer are hydrolyzed (the vesicle is sliced in half to reveal the inner leaflet phospholipids, which are not hydrolyzed).

Direct binding studies show that $sPLA_2$s bind several orders of magnitude tighter to vesicles that are anionic (such as vesicles of phosphatidylmethanol or mixed-lipid vesicles of phosphatidylcholine with phosphatidic acid or phosphatidylserine) compared with vesicles that are charge neutral (such as vesicles composed only of phosphatidylcholine) (16, 52, 54, 57, 60). The enzyme hydrolyzes these anionic vesicles in the scooting mode. With vesicles composed only of phosphatidylcholine, $sPLA_2$s catalyze interfacial reactions in a less processive mode in which the enzyme hops from one vesicle to another (57). In this case, the reaction progress curves are complex. The processivity and reaction velocity increase as the reaction progresses because accumulation of the fatty acid reaction product gives the vesicles a net negative charge that promotes enzyme binding (61). Kinetic modeling studies suggest that the complex reaction progress curve for the action of snake venom and pancreatic $sPLA_2$s on large unilamellar phosphatidylcholine vesicles results from dimerization of the enzyme bound to vesicles, and that this dimer persists as the enzyme hops from one vesicle to another (62). Enzyme dimerization, if it occurs, is not obligatory for interfacial catalysis as it has been conclusively shown that monomeric $sPLA_2$ is fully active on anionic vesicles in the scooting mode, and the enzyme does not aggregate even when multiple enzymes are present on each vesicle (53). $cPLA_2$s also undergo scooting mode catalysis on vesicles of phosphatidylcholine containing 5–10 mol % of reaction products (1:1 mixture of lysophospholipid and fatty acid (55). Numerous straightforward experimental protocols have been developed to analyze for scooting behavior (55, 63), and these are not discussed in this review.

Analysis of PLA_2s in the scooting mode provides the most straightforward method for proper analysis of the kinetics of interfacial catalysis. For enzymes that operate in the aqueous phase, it is assumed in all kinetic treatments that each enzyme in the mixture "sees" the same global concentrations of substrates and products. This is not necessarily the case for interfacial enzymes. Consider interfacial catalysis under conditions in which the processivity is low. At some point, a PLA_2 may leave a vesicle and bind to a new one that has not yet had a bound enzyme. This enzyme is effectively at time zero because it encounters only substrate and not products. In another instance, an enzyme may land on a vesicle that is mostly hydrolyzed; this enzyme is effectively at a long reaction time because it experiences product inhibition and substrate depletion. Thus, low processive catalysis leads to a scrambling of time, making kinetic analyses difficult, if not impossible, to interpret. This problem is eliminated by studying PLA_2s in the scooting mode. Consider the situation in which the enzymes are irreversibly bound to the vesicles and there is sufficient excess of vesicles over enzymes so that vesicles contain at most one bound enzyme. Now each enzyme-containing vesicle will be synchronized in time; at time zero the enzyme sees a full complement of substrate and at the end of the reaction the substrate in the vesicles has been depleted. Thus, the total product formed at any time is simply the amount of product formed in an enzyme-containing vesicle multiplied by the number of such vesicles.

The scooting mode analysis gives, at first glance, an artificial impression of interfacial catalysis, as under physiological conditions the PLA_2 may or may not be operating in a highly processive mode. However, for the reasons given above, the scooting mode analysis allows the kinetic and equilibrium constants that describe the interfacial catalysis to be measured, and these constants will apply to the action of the enzyme in the interface even if the enzyme is coming on and off the membrane. Under the conditions of low processivity, the interfacial kinetic and equilibrium parameters will be difficult to obtain as they are convoluted with the equilibrium constants that describe the binding of the enzyme to the interface; the latter can be measured directly by spectroscopic techniques (63). The problem is further complicated by the fact that the affinity of PLA_2s for the interface depends on the composition of the interface and thus on the fraction of substrate that has been converted to products. All these points have been discussed in detail elsewhere (57, 63, 64).

THE STRUCTURAL BASIS FOR SCOOTING MODE BEHAVIOR OF PLA_2

As stated in the introduction, X-ray structures are available for several $sPLA_2$s and, in some cases, with short-chain phospholipid analogs bound in their active sites. The structures reveal that the active site consists of a slot that traverses the enzyme into which a single phospholipid molecule can bind and interact with the catalytic residues (**Fig. 3**). This slot is clearly distinct from the surface of the enzyme that is thought to contact the bilayer (60). These structures and the kinetic results that demonstrate that the $E \rightarrow E^*$ step is distinct from the $E^* + S \rightarrow E^*S$ step (52, 60) suggest that a phospholipid molecule must diffuse about 15 Å from the plane of the bilayer into the enzyme bound to the interface in order to reach the catalytic machinery.

These high-resolution structures have also provided a wealth of information about the way in which the enzyme utilizes a histidine residue and a Ca^{2+} ion to help bind the substrate in the active site and to stabilize the substrate-derived transition state (8, 10).

TRUE COMPETITIVE INHIBITORS OF INTERFACIAL CATALYSIS BY PLA_2

The scooting mode analysis is also important for the proper analysis of reversible-binding, competitive inhibitors of PLA_2. History has shown that it is problematic to study reversible inhibitors of PLA_2 under conditions in which the enzyme is weakly bound to the interface (low processivity). This is because it is difficult to sort out whether an inhibitor is working by competing with the substrate for binding to the active site ($E^* + S \rightarrow E^*S$) or by altering the physical nature

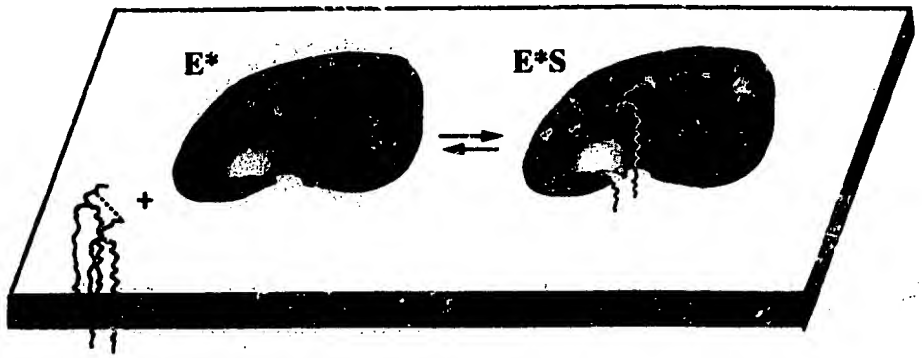


Figure 3. Movement of the substrate from the plane of the bilayer into the catalytic slot of the vesicle-bound $sPLA_2$. In the bottom-left corner are two phospholipids that interact via their polar head groups (dashed line). The polar head group of the phospholipid in the catalytic slot of the $sPLA_2$ is shown interacting with an amino acid side chain (dashed line); such an interaction occurs with the cobra venom $sPLA_2$ but not with the enzymes from pancreas, human synovial fluid, and bee venom.

of the interface so that more of the enzyme desorbs from the surface ($E^* \rightarrow E$). Many previously reported PLA_2 inhibitors have been shown to partition into vesicles and to decrease the fraction of enzyme bound to vesicles (65–67). The characteristics of such nonspecific and therefore uninteresting PLA_2 inhibitors are as follows: *1)* inhibition is seen when the enzyme is weakly bound to vesicles but not when the enzyme is tightly bound to vesicles (scooting mode); *2)* stereoisomers of inhibitors with chiral centers display similar inhibition potencies; *3)* large amounts of inhibitors (corresponding to more than a few mole % inhibitor in the vesicle) are needed to produce the inhibition. The last point is often overlooked. Many PLA_2 assays are carried out radiometrically with small amounts of phospholipid substrate (micromolar), and thus even nanomolar amounts of inhibitor can have a profound effect on the physical nature of the vesicle surface especially for inhibitors that partition favorably into vesicles (contrast this with the situation of enzymes that operate in the aqueous phase where the inhibitor and substrate do not form a coaggregate).

All these problems are avoided by analyzing putative PLA_2 inhibitors in the scooting mode. The presence of additives in anionic vesicles up to 10–20 mol % do not affect the kinetics of interfacial catalysis as the enzyme remains tightly bound to the interface (65). Instead, agents that bind specifically to the active site of the enzyme, the true competitive inhibitors of interfacial catalysis, are detected. The scooting mode analysis has been useful for conducting large-scale screens of compound banks for PLA_2 inhibitors as is routinely done at many pharmaceutical companies (68). Such an analysis does not detect false positive lead compounds that are often encountered in inhibitor screens. By using an assay in which the enzyme is tightly bound to the vesicle, possible inhibitors that bind specifically and tightly to the enzyme in the aqueous phase and prevent the enzyme from binding to the interface may be missed; this is a perfectly valid and useful mode of PLA_2 inhibition. However, the molecular surface of the PLA_2 that contacts the interface is large, and the membrane binding involves the interaction of several amino acids with the interface; thus, it is unlikely that an inhibitor will be able to mask a fraction of this surface sufficient to prevent the $E \rightarrow E^*$ step. Inhibitors that bind in the active site of the enzyme in solution but do not prevent the $E \rightarrow E^*$ step can also be imagined, but if such compounds are driven off the enzyme concomitant with the $E \rightarrow E^*$ step, the inhibitor will be useless. In other words, one is forced to search for inhibitors that may or may not bind to E but must bind to E^*. Thus, there is little merit in using inhibitor screening strategies that employ E acting on a water-soluble substrate. Other aspects of these arguments have been discussed previously (69).

The equation that describes the inhibition (*Eq. 1*) is a straightforward extension of the standard steady-state equation that describes competitive inhibition of enzymes that operate in aqueous solution:

$$v_o/v_o' = I = [(1 + 1/K_I^*)/(1 + 1/K_M^*)][X_I/(1 - X_I)] \quad (1)$$

Here, v_o and v_o' are the initial reaction velocities for the action of the enzyme in the scooting mode in the absence or presence of a competitive inhibitor, respectively. K_M^* is the interfacial Michaelis constant [just as K_M is the concentration (mol/l) of substrate in the aqueous phase that gives a reaction velocity of $V_{max}/2$, K_M^* is the mole fraction of substrate in the vesicle interface that gives $V_{max}/2$]. K_I^* is the interfacial dissociation constant for the E^*I complex (the mole fraction of I in the interface that gives $E^*/E^*I = 1$). Thus, the degree of inhibition depends on the affinity of the inhibitor and substrate to the enzyme (K_I^* and K_M^*) and the mole fraction of inhibition in the vesicle (X_I) [if the amount of inhibitor in the interface is significantly less than the amount of substrate in the vesicle, as is the case for tight-binding inhibitors, the $(1\text{-}X_I)$ term in *Eq. 1* can be ignored]. True competitive inhibitors of PLA_2 lead to kinetics that are consistent with *Eq. 1* (65, 66).

Phospholipids dispersed in detergent micelles have also been used as PLA_2 substrates and in the analysis of inhibitors (see, for example, refs 70–73). In these systems, tight-binding competitive inhibitors are revealed, and the degree of inhibition depends on the stereochemistry of chiral inhibitors, as is the case with vesicle assays. Some differences between mixed micelles and vesicle assays of inhibition may be noted. The binding of $sPLA_2$ to mixed micelles is typically of lower affinity than to anionic vesicles, and thus the mole fraction of inhibitor in mixed micelles should be kept low so that one avoids the problem of a shift in the E to E^* equilibrium as previously discussed. It is becoming apparent that reaction velocities for $sPLA_2$-catalysis lipolysis of mixed micelles is limited by the rate of substrate replenishment in enzyme-containing aggregates (74, 75). This stems from the

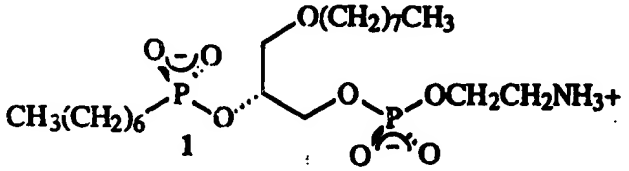
fact that mixed micelles, in contrast to vesicles, contain only a few substrate molecules, and thus significant substrate depletion occurs in the millisecond time scale. Interaggregate exchange of enzyme and/or phospholipid is required to maintain the reaction progress. Thus, it is possible to imagine an inhibitor that functions not by binding directly to E* but by slowing the rate of interaggregate exchange of substrate and/or enzyme. It may or may not be a valid assumption that such a concern will be avoided if the mole fraction of inhibitor in the aggregate is kept low. Finally, the process or rate-limiting substrate replenishment may distort the value of the mole fraction of inhibitor needed to cause 50% inhibition. This is because the local concentration of substrate in enzyme-containing mixed micelles will be lower than that in the bulk of the micelles that do not have bound enzyme. Thus, the mole fraction of inhibitor needed to cause a 50% reduction will be lower than that predicted by the true K_I^* value, because the inhibitor is competing with an artificially low amount of substrate present in enzyme-containing mixed micelles. This inequality is not possible if the rate of substrate replenishment is fast on the lipolysis turnover time scale so that the local and global steady-state substrate concentrations are equivalent. This situation is not a serious problem as values of K_I^* determined kinetically and under equilibrium conditions are correlated as expected (76).

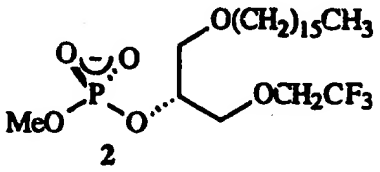
NEUTRAL DILUENTS

Because binding of the enzyme to the interface is independent of the binding of a molecule in the interface to the active site of the enzyme, it should be possible to find an amphiphile that forms an aggregate to which PLA_2 can bind but has no affinity for the active site of the enzyme and so E* has its active site filled with water. Such a compound has been termed a neutral diluent because it can be added to a vesicle of substrate phospholipid and thereby dilute the surface concentration of substrate that the bound enzyme "sees," and at the same time the neutral diluent does not inhibit the enzyme by binding to its catalytic site. The amphiphiles 2-hexadecyl-*sn*-glycero-3-phosphocholine and hexadecylphosphocholine are neutral diluents for pig pancreatic and human synovial sPLA2s, respectively (54, 65). This has been established by the demonstration that active site-directed alkylating agents (*p*-substituted phenacyl bromides) modify the catalytic histidine residue of the enzyme in the aqueous phase or bound to an aggregate of neutral diluent at the same rate, which shows that the active site is not protected from alkylation by the binding of the amphiphile. The use of a neutral diluent in combination with an active site-directed alkylating agent provides an independent measure of K_I^* values for PLA_2 inhibitors. This is because when a competitive inhibitor of PLA_2 is present in an aggregate of neutral diluent at mole fraction = K_I^*, half of the bound enzyme will be in the E*I form and the half-time for alkylation of the enzyme will be twice its value obtained in the absence of the inhibitor (65).

STRUCTURAL CLASSES OF REVERSIBLE, TIGHT-BINDING COMPETITIVE INHIBITORS OF PLA_2

Phospholipid analogs that have a phosphonate or phosphate in place of the ester at the *sn*-2 position of phospholipids (compounds 1 and 2 (below) are tight-binding inhibitors of $sPLA_2$s but not $cPLA_2$s (54, 77–79). These substrate analogs are patterned after the putative tetrahedral intermediate that





forms when a water molecule attacks the substrate *sn*-2 ester; they bind to E* about three orders of magnitude tighter than substrates. The X-ray structures of sPLA2s containing bound compound 1 suggest how the lipolysis reaction is catalyzed (8, 15) (**Fig. 4**). One nonbridging oxygen of the phosphonate is hydrogen bonded to the protonated imidazole ring of the active site histidine, and the other is directly liganded to the calcium ion. This suggests that the mechanism of substrate hydrolysis involves the attach of a water molecule onto the ester carbonyl carbon assisted by general base catalysis by histidine. The oxyanion, which is derived from the carbonyl oxygen, is stabilized by binding to calcium. The calcium also helps to anchor the substrate in th

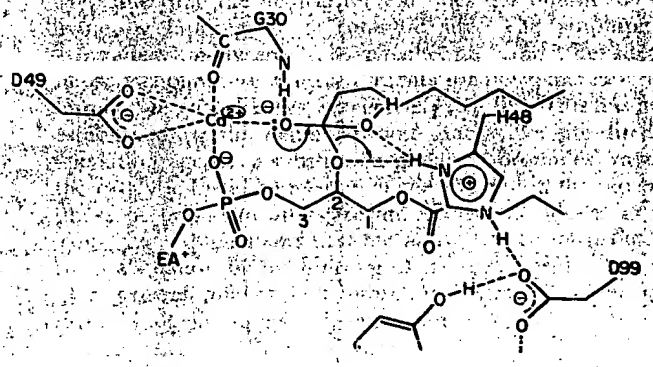


Figure 4. The structural details of the interaction of the putative tetrahedral intermediate with the catalytic residues of $sPLA_2$s as revealed by X-ray diffraction. The oxyanion of the tetrahedral intermediate interacts with calcium and the amide NH of glycine-30 (pancreatic $sPLA_2$ residue numbering). The hydroxyl group of the tetrahedral intermediate is hydrogen bonded to the protonated histidine; this amino acid likely protonates the *sn*-2-oxygen as the lysophospholipid is formed. The histidine is also hydrogen bonded to aspartate-99, which receives a hydrogen bond from a tyrosine residue. The *sn*-3-phosphate is liganded to the calcium; the latter is held to the enzyme by aspartate-49 and glycine-30, as shown, as well as two additional carbonyl oxygen ligands from the peptide backbone.

active site by its interacti n with one of the nonbridging oxygens of the *sn*-3 phosphate; the other nonbridging oxygen of this phosphate is hydrogen bonded to either a tyr sine (pancreatic and cobra venom $sPLA_2$s), a threonine (bee venom $sPLA_2$), or a lysine (human synovial fluid sPLA).

Compound 2 is a member of a novel family of phospholipid analogs that are tight-binding inhibitors of $sPLA_2$s (79). These compounds have an *sn*-2 phosphate but lack one at the *sn*-3 position. Apparently the polar head group of a phospholipid is not a critical element for its interaction with the active site of $sPLA_2$s even though it forms interactions with the active site as described in the previous section. This is also apparent from the following additional inhibitor studies. Analogs of phospholipids in which the *sn*-2 ester is replaced by an amide (-CONH-) are tight-binding inhibitors of $sPLA_2$s (70, 71, 80). The amide hydrogen is hydrogen bonded to the nonprotonated imidazole ring of the active site histidine, and the *sn*-3 phosphate is liganded to the calcium (10, 72). Surprisingly, simple fatty acid amides ($RCONH_2$) that lack the entire glycerol backbone bind to $sPLA_2$s with affinities approaching those of phospholipid amide analogues (discussed below) (68).

None of the $sPLA_2$ inhibitors described cause detectable inhibition of $cPLA_2$. However, an analog of arachidonic acid in which the COOH group is replaced with a trifluoromethyl ketone ($COCF_3$) is a tight-binding, reversible inhibitor of $cPLA_2$; this compound ($AACOCF_3$) is more than 1,000-fold less potent as an inhibitor of $sPLA_2$s (73). NMR studies suggest that $AACOCF_3$ forms a hemiketal adduct with an active site nucleophile [Enz-X-C(OH)(CF_3)-AA] (81). Such an adduct may resemble the tetrahedral intermediate in route to a putative acyl enzyme, but further studies will be required to fully understand the mechanism of catalysis by $cPLA_2$. Analogs of $AACOCF_3$ in which the $COCF_3$ group is replaced by $COCH_3$, $CH(OH)CF_3$, or $CONH_2$ are not $cPLA_2$ inhibitors (73). A possible reason for the ability of inhibitors that lack a phospholipid-like polar head group to bind tightly to $sPLA_2$ and $cPLA_2$ is discussed in the next section.

DIFFERENTIAL INTERACTIONS OF INHIBITORS WITH THE PHOSPHOLIPID INTERFACE AS A CONTROLLING FACTOR FOR POTENCIES OF PLA_2 INHIBITORS

In considering the factors that determine the magnitude of enzyme-inhibitor dissociation constants, one must examine not only the interactions that the inhibitor engages in with the enzyme but also the interactions that the inhibitor forms with its environment when it is not bound to the enzyme. For enzymes in the aqueous phase, experimental and theoretical studies have shown that differential solvation of inhibitors can dictate their relative affinities for enzymes (see, for example, ref 82). Thus, compound A may be a better inhibitor than B not because it forms stronger interactions with the enzyme than B but because as a free species it is less solvated than free B. The same is true for inhibitors of PLA_2, except that the free inhibitor is now in a lipid vesicle instead of in aqueous solution. Thus, differential interactions of inhibitors with adjacent phospholipid molecule in the vesicle can control, in part, the relative affinities f inhibitors for PLA_2 b und to the vesicle surface.

A systematic study was carried out on the effect of varying the structure of the polar head group of *sn*-2 phosphonat - c ntaining phosph lipid analogs on the binding to $sPLA_2$s (83). The inhibitor potencies were obtained according to *Eq. 1* and for the acti n of a number of $sPLA_2$s n vesicles of 1,2-dimyristoyl-*sn*-glycero-3-phosphomethanol in the scooting mode. When comparing inhibitors of PLA_2, it is important to determine whether all of the inhibitors are fully partitioned into the vesicle, otherwise the differences in inhibitor potencies may reflect differences in surface concentrations of inhibitor due to differential partitioning rather than differences in intrinsic affinities of the inhibitors for the enzyme (K_I^*). The scooting mode analysis provides a simple way to assess inhibitor partitioning. The degree of inhibition by a fixed mole fraction of inhibitor in the vesicle is determined at different total reaction volumes. Because the enzyme is tightly bound to the vesicles, the reaction velocity in the absence of inhibitor is independent of the reaction volume. If an inhibitor is present and if it is only partially partitioned into the vesicle phase, the degree of inhibition will decrease as the reaction volume is increased because the latter change will lead to a decrease in the mole fraction of inhibitor in the interface as more and more of it partitions into the aqueous phase. By this criterion, it has been shown that the differences in inhibitor potencies reflect differences in their values of K_I^* (83). A more direct method for determining inhibitor/vesicle partition coefficients has also been reported (84).

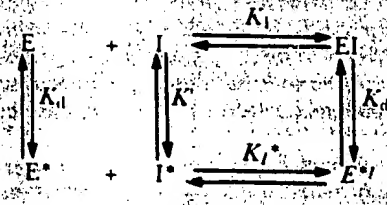
An interesting trend was discovered from this analysis. In the case of the $sPLA_2$s from porcine and bovine pancreas, bee venom, and human synovial fluid, replacement of the ammonium of the polar head group compound 1 with hydrogen increases the potency by 5- to 10-fold. In contrast, such a change produces no effect on the K_I^* measured with the cobra venom $sPLA_2$ (83). X-ray structural studies of $sPLA_2$-inhibitor complexes show that for the enzymes from pancreas, bee venom, and human synovial fluid, the ammonium of the phosphoethanolamine polar head group of the bound phospholipid analog does not directly contact the enzyme. Thus, the increase in inhibitor potency when the ammonium is removed must be because the ammonium group of the free inhibitor forms favorable interactions with the head group phosphate of an adjacent phospholipid in the vesicle; such an interaction is not possible with the analog lacking the ammonium group (Fig. 3). By analyzing the relative binding energies of a series of inhibitors with modified polar head groups to certain $sPLA_2$s, it is possible to determine the relative energetics of intermolecular polar head group interactions of phospholipids in bilayered vesicles. In the case of the cobra venom enzyme, removing this ammonium group breaks the interaction of the inhibitor with the enzyme (Fig. 3) and with the bilayer; thus, such a change is expected to produce little, if any, effect on the K_I^* values, as is observed.

E* HAS INTRINSICALLY HIGHER AFFINITY FOR INHIBITORS COMPARED WITH E

The binding of phospholipid analogs containing short hydrocarbon chains to PLA_2 in the aqueous phase can be studied because such compounds are water soluble as solitary monomers below their critical micelle concentrations or solubility limit. The apparent affinity of phosphonate phospholipid analog 1 for cobra venom $sPLA_2$ in the aqueous phase increases enormously in the presence of the nonhydrolyzable short-chain substrate anal g 1,2-dihexyl-*sn*-glycero-3-ph sphocholine (35). In this study, the binding f radiolabeled inhibitor 1 to cobra venom $sPLA_2$ was measured by equilibrium dialysis, and the K_I for the enzyme-inhibitor complex is about 50 μM. Thus, in the aqueous

phase, compound 1 acts as a rather weak-binding inhibitor. The addition of 1,2-dihexyl-*sn*-glycero-3-phosphocholine to the water-soluble cobra venom enzyme leads to the formation of a protein/lipid microaggregate that can be detected by gel filtration or analytical ultracentrifugation (86–88). Aggregation is also seen with the pancreatic $sPLA_2$ in the presence of short-chain anionic amphiphiles (89, 90). These aggregates presumably form by the ability of the interfacial recognition surface of the PLA_2 to recruit short-chain, water-soluble phospholipids in a process that leads to the segregation of such complexes to form a protein-lipid microaggregate. Thus, in the presence of 1,2-dihexyl-*sn*-glycero-3-phosphocholine, the cobra venom PLA_2 may have the properties more of E* than of E. The fact that the inhibitor binds more tightly to the enzyme in the presence of this microaggregation suggests that E* has intrinsically higher affinity for E* than does E.

These results are only qualitative, and they have sparked the design of additional and more rigorous experiments that address the intrinic affinity of E vs. E* for active site ligands (84). One problem that immediately arises is that it is not possible to directly compare the values of K_I (for the process EI < > E + I) to K_I^* (for the process (E*I < > E* + I*), as the former has units of molarity and the latter has units of mole fraction. Instead it is most useful to consider these equilibrium processes in terms of Scheme II shown below.



Scheme II

In this scheme all the underlying equilibria are considered for the interaction of the inhibitor with the enzyme both in the aqueous phase and at the interface. Thus, in addition to the dissociation constants K_I and K_I^* discussed previously, the constants K_d and K_d^I are the equilibrium constants for the dissociation of E* and E*I, respectively, from the interface of the neutral diluent into the aqueous phase. Thus, K_d = [neutral diluent][E]/[E*] and K_d^I = [neutral diluent][EI]/[E*I] where quantities in brackets are in units of moles per unit volume. The remaining constant, K', is the equilibrium constant for the dissociation of the inhibitor from the interface into the aqueous phase (K' = [neutral diluent][I]/[I*]).

Equation 2 is a thermodynamic relation (detailed-balance condition) derived from Scheme II.

$$K_d/K_d^I = K_I/(K_I^* K') = [E][E^*I]/[E^*][EI] \quad (2)$$

According to this equation, if $K_d/K_d^I > 1$, $[E^*I]/[E^*] > [EI]/[E]$, and thus regardless of the total amount of inhibitor in the system, the fraction of enzyme in the interface that is bound to inhibitor is higher than that for the enzyme in the aqueous phase. Using the thermodynamic cycle (Scheme II) in this way provides a direct evaluation of the intrinsic inhibitor affinity and automatically accounts for differences in local concentrations of inhibitor in the aqueous phase and at the interface.

For all true competitive inhibitors of the pig pancreatic $sPLA_2$ studied, it is found that K_d/K_d^I is approximately 50 (84). This strengthening of the enzyme-interface binding could come about in three different ways: *1)* It could be due to a residual inhibitor-interface interaction where part of the inhibitor remains attached to the interface even when the inhibitor has entered the catalytic site; *2)* The interface could somehow be influenced by the inhibitor moving into the catalytic site so that it makes better contact with the enzyme; *3)* The enzyme may undergo a conformation change when the inhibitor binds so that it makes better contact with the interface. The first two possibilities would suggest that the length of the alkyl chains of the inhibitors would influence the strength of the effect; surprisingly, this is not the case (84). Thus, the most likely effect is an allosteric modulation of the enzyme that occurs when the inhibitor binds in the catalytic site.

PLA_2 INHIBITION STUDIES IN LIVING CELLS

Now that some PLA_2s in cells have been identified and true competitive inhibitors that are enzyme selective have been developed, it should be possible to take a pharmacological approach toward determining the roles that these enzymes play in biological processes. Of course, such an approach does not provide unequivocal data because unidentified PLA_2s may exist in cells, and the full spectrum of enzyme selectivity of any given inhibitor is not known a priori.

The presence of $AACOCF_3$ at concentrations of 0–20 μM blocks essentially all the arachidonic acid that is liberated in thrombin-stimulated platelets (91, 92), in calcium ionophore-stimulated human monocytic cells (U937) (92), and in interleukin 1α-stimulated mesangial cells (93). However, such effects are not seen when the cells are treated with analogs of $AACOCF_3$, which have minor structural alterations that obliterate their abilities to inhibit $cPLA_2$ (see above). Such results argue strongly for the role of the $cPLA_2$ in liberating arachidonate for the biosynthesis of eicosanoids. Furthermore, they allay concerns about using membrane-residing inhibitors to inhibit the action of $cPLA_2$ in membranes.

Phospholipid analog 2 protects isolated rat lungs from ischemia reperfusion injury when it is delivered as a suspension in liposomes, whereas micelles of this compound added directly to the perfusion medium are ineffective (36). Compound 2 also inhibits the degradation of surfactant phosphatidylcholine by rat lung (94). Biochemical studies suggest that the primary inhibitory effect of this compound is on a calcium-independent PLA_2 of lysosomal origin with optimum activity at acidic pH. This activity is probably involved in the turnover of phospholipids of lung surfactant. This enzyme not only hydrolyzes normal phospholipids but is also responsible for the selective release of conjugated dienes and thiobarbituric acid reactive substances; however, the phospholipid cleavage leading to the formation of thromboxane is not affected.

A substituted bromoenoyl lactone is a specific inhibitor of the calcium-independent PLA_2 from myocardium, and this compound blocks arachidonate liberation in hormone-stimulated arterial smooth muscle cells (51). FJ

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Periodicity of leucine and tandem repetition of a 24-amino acid segment in the primary structure of leucine-rich α_2-glycoprotein of human serum

(protein structure/amphiphilic structure/gene duplication/membrane protein/galactosamine and glucosamine oligosaccharides)

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ABSTRACT **The complete primary structure of the 3.1S leucine-rich α_2-glycoprotein (LRG) present in human plasma has been determined. This protein (M_r ≈45,000) consists of a single polypeptide chain with one galactosamine and four glucosamine oligosaccharides attached. The polypeptide has two intrachain disulfide bonds and contains 312 amino acid residues of which 66 are leucine. The amino acid sequence can be exactly divided into 13 segments of 24 residues each, eight of which exhibit a periodic pattern in the occurrence of leucine, proline, and asparagine. The consensus sequence for the repeating tetracosapeptide unit is Pro-Xaa-Xaa-Leu-Leu-Xaa-Xaa-Xaa-Xaa-Xaa-Leu-Xaa-Xaa-Leu-Xaa-Leu-Xaa-Xaa-Asn-Xaa-Leu-Xaa-Xaa-Leu. This periodicity suggests that the unique structure of LRG arose from a series of unequal crossovers of a precursor oligonucleotide sequence that encoded a building block rich in leucine. Overall, the amino acid sequence of LRG is not significantly homologous to the continuous sequence of any protein in the current data base. However, the consensus tetracosapeptide sequence shows strong homology to segments of many mitochondrial proteins, viral envelope proteins, and oncogene proteins that have a high leucine content and transmembrane domains. Tandem repetition of similar segments also occurs in apolipoproteins that have amphipathic helical potential. Prediction of the secondary structure by the Chou–Fasman rules and calculation of the hydrophilic/hydrophobic profile by several methods confirm the tandem repetition of largely hydrophobic structural units; these begin with a β-turn that leads into an organized structure with α-helical or β-sheet potential. These structural characteristics and the homology to mitochondrial proteins and apolipoproteins suggest that LRG is a membrane-derived or membrane-associated protein containing a series of domains capable of bipolar surface orientation.**

Although complete amino acid sequences have been reported for about half of the nearly 100 proteins that have been isolated from human plasma (1), little is known about the structure of a series of well-characterized α- and β-glycoproteins of uncertain or unknown function (2). We have begun study of some of these as part of a program for investigation of the structure and function of human plasma proteins (3, 4). We report here the complete amino acid sequence of a trace component of unknown function that was isolated from human serum in 1977 by Haupt and Baudner (5). They called it 3.1S leucine-rich α_2-glycoprotein (LRG) because of its sedimentation coefficient, its unusually high content of leucine, and its electrophoretic mobility. The protein was reported to consist of a single polypeptide chain (M_r ≈ 50,000) and to contain about 23% carbohydrate by weight (5). To our knowledge, no other structural data have since been published.

LRG is a trace protein of human plasma. The average content of LRG in adult serum is 2.1 mg/100 ml (5). Although neither the site of synthesis nor the function are known and no relationship to disease has been reported, LRG is of interest because of its unusually high content of leucine, which is about 17% by weight. Thus, about every fifth residue is leucine. Whether the leucine is randomly distributed or occurs in a regular structural pattern could only be determined by amino acid sequencing, which we undertook and completed. We found that the sequence exhibits a novel periodic pattern unlike that previously reported for soluble globular proteins except apolipoproteins (6–8). The single polypeptide chain is composed of 312 amino acid residues, and the sequence can be exactly divided into 13 blocks of 24 residues; eight of these tetracosapeptide sequences exhibit a periodic pattern in the distribution of leucine and certain other residues. The periodic pattern is highly significant statistically; the segment comparison score in SD units for the top 100 scores is 18.06. This suggests that LRG arose by a series of unequal crossovers of an oligonucleotide sequence that encoded a prototype leucine-rich building block of about 24 amino acid residues.

The periodicity in the primary structure of LRG is due to a recurring pattern of leucine residues that produces a segment similar in hydrophobicity and length to that found in the transmembrane segments of amphiphilic (amphipathic) peptides and proteins (9, 10). Thus, we suggest that LRG may be a membrane-associated or membrane-derived protein. This hypothesis is supported by predictions of the secondary structure and the hydrophilic/hydrophobic character (hydropathy profile) of the polypeptide chain.

MATERIALS AND METHODS

Materials. Purified LRG prepared from human serum by the method of Haupt and Baudner (5) and antiserum specific for LRG were obtained from Behringwerke AG (Marburg/Lahn, F.R.G.). The protein migrated as a single band in Na-DodSO$_4$/polyacrylamide gel electrophoresis both in the presence and absence of 2-mercaptoethanol.

Methods. Methods used for the determination of the primary structure of proteins in our laboratory have been described (3, 4, 11). The purified LRG was reduced and carboxymethylated before sequence analysis. The carboxymethylated protein (5–15 mg) was subjected to separate digestions with L-1-tosylamido-2-phenylethyl chloromethyl ketone-treated trypsin, *Staphylococcus aureus* V8 protease, and endoproteinase Lys-C. The intact protein was also

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Abbreviation: LRG, leucine-rich α_2-glycoprotein.

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cleaved with dilute acid at 108°C for 4 hr (12). Each enzymatic digest was separated by a combination of gel filtration and high-performance liquid chromatography (HPLC) on an Ultrasphere ODS column (Altex, Berkeley, CA) or a Synchropak RP-P column (SynChrom, Linden, IN) with a programmed gradient of 1-propanol containing 0.1% trifluoroacetic acid or 0.1% heptafluorobutyric acid (4). The digest with dilute acid was separated by an automated two-step HPLC system; this consists of a combination of anion-exchange chromatography with a Spherogel-TSK IEX-540 DEAE column (Altex) as the first step and chromatography with a reversed-phase Ultrasphere ODS column as the second. The purified peptides were analyzed with the amino acid analyzer, and their sequences were determined by automatic Edman degradation (3, 4, 11). Hexosamine analysis was also done with the amino acid analyzer, after acid hydrolysis (3, 11).

Computer Analysis of Sequence Data. The sequence data base of the *Atlas of Protein Sequence and Structure* updated to August 1984 and the programs SEARCH, ALIGN, RELATE, and PRPLOT were provided by the National Biomedical Research Foundation.† The programs SEARCH, RELATE, and ALIGN (13) were used either with the unitary matrix or with the mutation data matrix; all gave a score for statistical significance in standard deviations (SD) of the real score above a score of 100 random runs. We used PRPLOT to plot the hydrophilic/hydrophobic profile of the molecule by utilizing different scales including those of Kyte and Doolittle (14), Wolfenden *et al.* (15), Argos *et al.* (16), and Eisenberg (10). PRPLOT was also used to estimate the secondary structure predicted by the procedure of Chou and Fasman (17) based on their values for the tendency of individual amino acids to appear in α-helix, β-sheet, and β-turn structures.

RESULTS AND DISCUSSION

Amino Acid Composition. The amino acid composition calculated from the sequence analysis (Table 1) corresponds well with that obtained by amino acid analysis of the protein (5). The very high content of leucine (66 of 312 residues) is an unusual characteristic of this protein. By amino acid analysis the leucine content of the glycoprotein is 16.62% by weight (5). The value for the polypeptide portion calculated from the complete sequence is 21.75% by weight or 21.12 mole %. A search of the protein sequence data base† showed that the leucine content of LRG is exceeded only by those of a vespid venom peptide, a few hypothetical bacteriophage and mitochondrial proteins corresponding to gene sequences, and the hormone secretin. Most other sequences listed that had a high leucine content (15–20 mole %) also were for hypothetical mitochondrial proteins or were for known mitochondrial cytochromes and enzymes, viral coat proteins, or biologically active peptides. About one-third of the amino acid residues of LRG are strongly hydrophobic. Other notable features are the low content of tyrosine (3 residues), isoleucine (4 residues), and cysteine (4 residues). The latter are linked in two disulfide bonds; one is close to the amino terminus and is between cysteine-8 and cysteine-21, and the other is near the carboxyl terminus and is between cysteine-268 and cysteine-294.

Polypeptide Structure and Molecular Weight. Human LRG consists of a single polypeptide chain containing 312 amino acid residues, one GalN oligosaccharide, and four GlcN oligosaccharides (Fig. 1). The M_r calculated for the unglycosylated polypeptide chain is 34,346. An M_r of 35,970 was obtained from electrophoresis in $NaDodSO_4$/polyacrylamide gels when the results estimated in gels ranging from 5% to 20% gel concentration were extrapolated by use of a double-reciprocal plot. This value, which presumably reflects only the polypeptide chain, is much less than the M_r of 49,600 ± 4,000 determined by equilibrium sedimentation (5). However, the carbohydrate content of LRG (about 23% by weight) contributes significantly to the M_r and also makes it difficult to determine the M_r accurately by physicochemical methods. We estimate that the M_r of LRG is approximately 45,000, based on the value of 34,346 for the polypeptide portion and an estimate of 600 for the GalN oligosaccharide and of 2500 for each of the four GlcN oligosaccharides.

Table 1. Amino acid composition of human LRG based on the complete amino acid sequence determination

Amino acid	No. of residues	Amino acid	No. of residues
Aspartic acid	19	Valine	14
Asparagine	17	Methionine	3
Threonine	12	Isoleucine	4
Serine	21	Leucine	66
Glutamic acid	14	Tyrosine	3
Glutamine	20	Phenylalanine	10
Proline	22	Lysine	12
Glycine	23	Histidine	7
Alanine	21	Arginine	15
Half-cystine	4	Tryptophan	5

M_r of unmodified polypeptide chain is 34,346; number of residues is 312. Thr-2 is linked to a GalN oligosaccharide. Asn-44, Asn-151, Asn-234, and Asn-290 are linked to GlcN oligosaccharides.

Number and Location of Oligosaccharides. Fig. 1 gives the complete amino acid sequence of LRG and shows the sites of attachment of the five oligosaccharides. The GalN is O-linked to the second residue (Thr-2). Both in its proximity to the amino terminus and to a nearby proline, this linkage is similar to that of the GalN attached to the amino-terminal residue (threonine) in human hemopexin (11, 18). However, no obligatory signal sequence for the attachment of GalN is known, whereas GlcN is always N-linked to asparagine in the tripeptide sequence Asn-Xaa-(Thr/Ser). In LRG there are four GlcN oligosaccharides; these are linked to Asn-44, Asn-151, Asn-234, and Asn-290. However, the asparagine is not glycosylated in the putative acceptor sequence Asn-Leu-Ser at positions 271–273. Nothing has been published about the carbohydrate structure of the oligosaccharides of LRG; however, a complex dibranched GlcN oligosaccharide is the most common carbohydrate in human plasma glycoproteins (19).

Internal Homology. Although many plasma proteins exhibit strong evidence of internal duplication in amino acid sequence (20, 21), at first appearance LRG does not. Despite the frequency of leucine residues, there are only five instances of a Leu-Leu sequence and only one case of the triplet sequence Leu-Leu-Leu, compared to 53 instances of single leucine residues. This lack of a statistical distribution puzzled us. However, first by visual inspection and then by computer analysis with the program RELATE, we found that the amino acid sequence of LRG fits a 13-cycle periodic pattern dominated by a 24-residue peptide (tetracosapeptide) which has the consensus sequence Pro-Xaa-Xaa-Leu-Leu-Xaa-Xaa-Xaa-Xaa-Xaa-Leu-Xaa-Xaa-Leu-Xaa-Leu-Xaa-Xaa-Asn-Xaa-Leu-Xaa-Xaa-Leu. All of the amino acid residues identified in this sequence occur at least six times in the alignment shown in Fig. 2. In the computer listing of the 100 segments having the highest scores for intrasequence homology (the top 100 of 39,903 comparisons), the lengths of all

†Barker, W. C., Hunt, L. T., Orcutt, B. C., George, D. G., Yeh, L. S., Chen, H. R., Blomquist, M. C., Johnson, G. C. & Dayhoff, M. O. (Aug. 1, 1984) *Atlas of Protein Sequence and Structure*, Protein Sequence Database, (Natl. Biomed. Res. Found., Washington, D.C.).

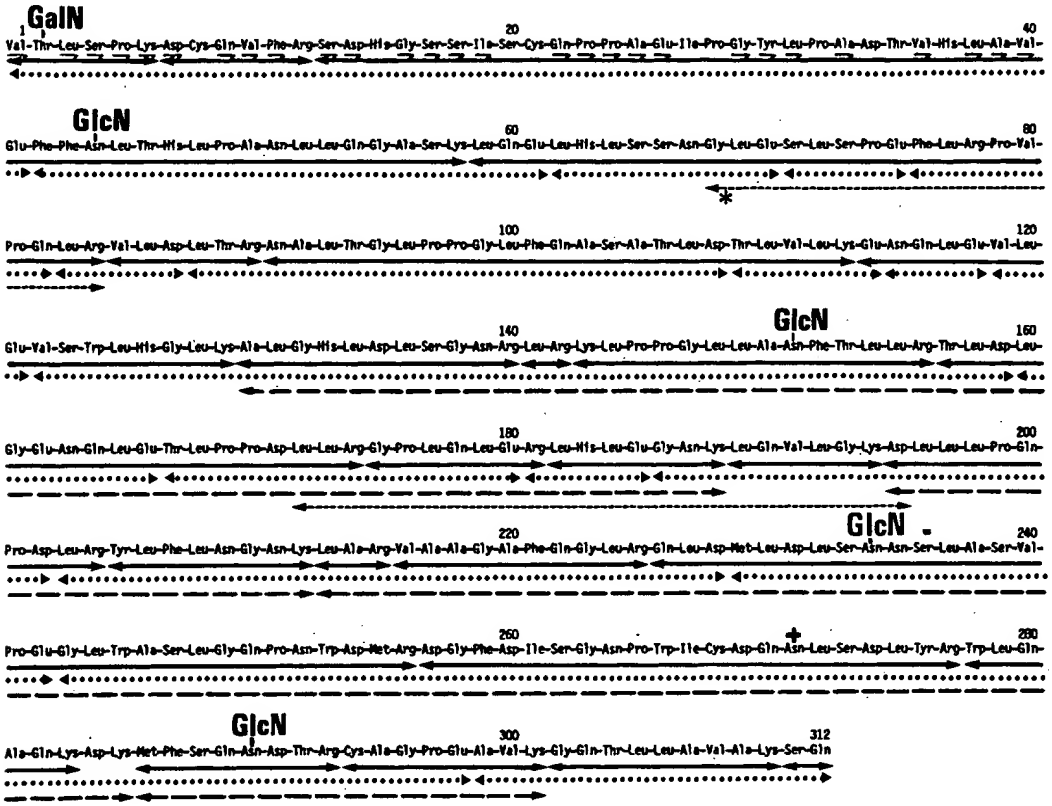

FIG. 1. Summary of the complete amino acid sequence of human LRG. The sequence is shown along with all peptides necessary for the proof of sequence. The peptides obtained from different digestions are as follows: ———, tryptic peptides; ·····, *S. aureus* V8 peptides; – – –, endoproteinase Lys-C peptides; – · – · –, dilute acid peptides. The asterisk indicates a dilute acid peptide of a tryptic peptide. GalN and GlcN indicate the attachment sites for the galactosamine oligosaccharide and the glucosamine oligosaccharides, respectively. A potential glycosylation site (Asn-271) is shown by a plus sign. No evidence for polymorphism in the sequence of LRG was found except for a possible ambiguity at position 215, where tyrosine may replace arginine in some molecules.

segments listed were divisible by 24, and all the segments fit exactly into the periodic pattern of Fig. 2. In this pattern, the complete sequence of 312 residues is exactly divided into an array of 13 tetracosapeptide segments with no gaps inserted. The segment comparison score for the tetracosapeptide segments is 18.06 SD units. A score of 3.0 SD units is considered significant (13).

The unique feature of the 13-cycle alignment is that it is based mainly on a periodic distribution of a single amino acid rather than on a recurrent sequence of several different amino acids. More than 50 of the 66 leucine residues fit the pattern, including almost all the leucines in the 200 successive residues (nos. 38–237) in which the most homologous tetracosapeptide segments are located. Four more leucines are aligned in column 8 of Fig. 2. Since leucine is one of the most hydrophobic amino acids and is usually present in an or-

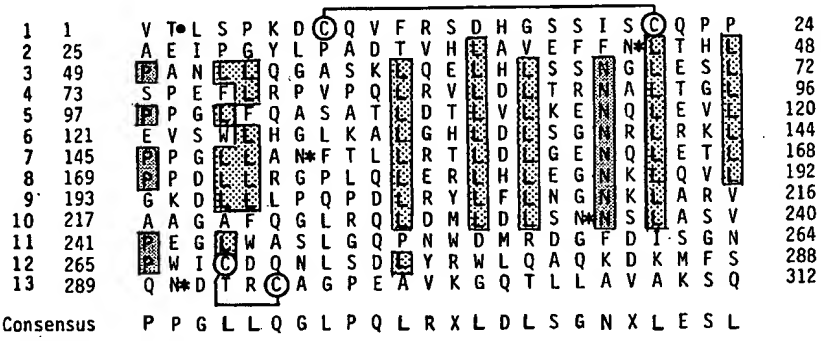

FIG. 2. Periodicity of leucine residues and tandem repetition of a 24-amino acid segment in the primary structure of LRG. The sequence of Fig. 1 with position numbers is shown in the one-letter code for amino acids (13) and is aligned exactly into 13 segments (numbered in bold type). Amino acids that occur at least six times in a vertical column are shown in bold type and are enclosed in shaded boxes. The consensus sequence is given at the bottom, with the most frequent residues in bold type. Others that occur three or four times are also given in the consensus sequence, and X is used where there is no clear preference. The cysteine (C) residues are circled and the disulfide bonds are represented schematically. An asterisk denotes each asparagine (N) to which a GlcN oligosaccharide is linked, and a solid circle at threonine-2 indicates that a GalN oligosaccharide is attached.

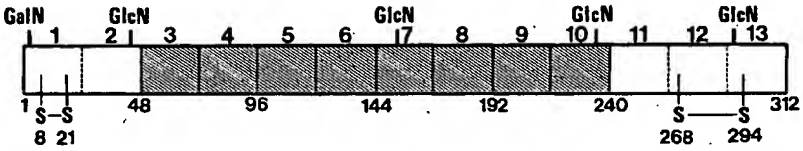

FIG. 3. Schematic representation of the tandem repetition of 24-amino acid segments in LRG. Each numbered block represents a segment (see Fig. 2). Shaded blocks represent homologous segments that exhibit a periodic pattern of leucine and other amino acids. The numbers below the diagram give the sequence positions. The locations of the GalN and GlcN oligosaccharides and of the two disulfide bonds are shown.

dered structure (α-helix or β-pleated sheet), the periodicity of leucine residues probably reflects a unique structural characteristic of LRG that has been attained by a series of unequal crossovers of an oligonucleotide sequence that coded for a prototype building block that was rich in leucine. Although the entire polypeptide sequence is exactly divisible into 13 tetracosapeptide segments, only the central 8 segments exhibit strong inter-segment homology. These comprise a central core structure, illustrated schematically in Fig. 3. The amino-terminal segment has a GalN oligosaccharide and an intra-segment disulfide bond. The periodic pattern of homology ends after segment 10. The last two segments are joined by a disulfide bond, and the last has a GlcN oligosaccharide.

Sequence Homology to Other Proteins. To examine the possible occurrence in other proteins of sequences homologous to the periodic tetracosapeptide of LRG, we used as a probe a consensus sequence that represents the amino acid of highest frequency in each vertical column of Fig. 2. The sequence used was Pro-Pro-Gly-Leu-Leu-Gln-Gly-Leu-Pro-Gln-Leu-Arg-Xaa-Leu-Asp-Leu-Ser-Gly-Asn-Xaa-Leu-Glu-Ser-Leu, in which Xaa indicates that no amino acid occurred with sufficient frequency.

By use of the program SEARCH and both the unitary matrix and the mutation data matrix, we found that LRG has a unique amino acid sequence that does not exhibit significant homology over a series of contiguous segments to any protein in the current sequence data base.† However, most of the repeating tetracosapeptide segments of LRG do exhibit striking homology of their basic pattern with segments of a number of polypeptides, most of which have a high leucine content. These polypeptides include many viral envelope proteins, oncogene products, and a number of known mitochondrial proteins, such as various cytochromes as well as hypothetical mitochondrial proteins for which the sequences have been deduced by cloning techniques. For example, when the unitary matrix was used, the highest score for the prototype tetracosapeptide sequence was given by a 24-residue segment of hypothetical protein 4 of the human mitochondrion, which has a leucine content of 21 mole % (22). Other segments of protein 4 and other mitochondrial proteins scored high, but the matching segments were not contiguous in the sequences of the proteins. When the mutation data matrix was used, the highest score was for the hemagglutinin precursor of various strains of human and duck influenza virus (residues 441–464). This segment corresponds to residues 78–101 in the second (HA_2) chain of the processed virus protein and exists as a long α-helix with a 36-Å hydrophobic exterior surface (23).

We do not suggest that the homology identified signifies a genetic or evolutionary relationship. Rather, it probably reflects the fact that a high leucine content may result in a periodicity in sequence similar to that of LRG. In an organized structure such as the α-helix or β-pleated sheet (for both of which leucine has a high potential), the hydrophobic residues tend to cluster in a similar orientation (9, 10). Such hydrophobic patches must either be in the interior of protein molecules or, if on the exterior, will tend to interact with hydrophobic membrane surfaces.

The high solubility of LRG and its resistance to heat coagulation are probably due to the combination of a high carbohydrate content, which greatly increases the hydrophilicity of the protein surface, and to the clustering of the hydrophobic leucine residues, which are probably internalized in the protein.

Tandem Repetitions of Protein Sequences. Although fibrous proteins such as collagen have frequent short (tripeptide) repeating units, tandem repetitions of the length and type found in LRG are rare. However, some apolipoproteins contain a series of 11-amino acid or 22-amino acid segments similar to although not closely homologous with the repeating sequence in LRG (6–8). Fitch (6) identified a 13-cycle repeat of an 11-amino acid (or 22-amino acid) sequence in human apolipoprotein A-I and proposed that it resulted from a series of intragenic unequal crossovers. Barker and Dayhoff (7) identified a similar periodicity in human apolipoproteins A-II, C-II, and C-III and suggested that the four lipoproteins arose from a single ancestral gene. Recently Boguski *et al.* (8) reported that rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino acid segment with amphipathic helical potential. The consensus sequence of the apolipoproteins is similar to that of LRG in length, in the number of repetitions, and in the frequency of leucine and other hydrophobic residues. However, the sequence homology of LRG and apolipoproteins is not pronounced; hence, they probably have a functional rather than a genetic relationship. The apolipoprotein repeating sequence can be drawn as an α-helical wheel with amphiphilic character; that is, the nonpolar residues are segregated on one section of the circumference, and hydrophilic and charged residues are aligned on the rest. The Chou–Fasman rules (17) lead to the prediction of an alternating secondary structure, which is in accord with a plot of the hydropathic index. The result is a helical amphiphilic structure to which the function of lipid binding is attributed.

Hydrophilic/Hydrophobic Profile. When the computer program PRPLOT was used with different scales (10, 14–16) to evaluate the hydrophilic/hydrophobic profile of LRG, the results were in general agreement. Computation of the hydropathic index of Kyte and Doolittle (14) (Fig. 4) shows that the eight conserved segments of the central core are largely hydrophobic, whereas the amino-terminal segment and the last two segments are mainly hydrophilic. Each of the central eight segments has a predominantly hydrophobic pattern with a short hydrophilic section in the middle or near the carboxyl terminus. The patterns for the eight tandem segments are similar but not identical. The carboxyl-terminal segment appears to end with a hydrophobic segment; this could be buried inside the molecule, or it could be a transmembrane segment. In view of the high leucine content, the hydrophobicity of LRG is not unexpected. However, using the method of Eisenberg (10), we were unable to identify a series of potential membrane segments of 21–24 residues in length, such as those he described in some membrane proteins. Also, the periodic leucine residues did not all cluster together in an α-helical wheel as the hydrophobic residues tend to do in apolipoproteins and amphiphilic peptides (8–10).

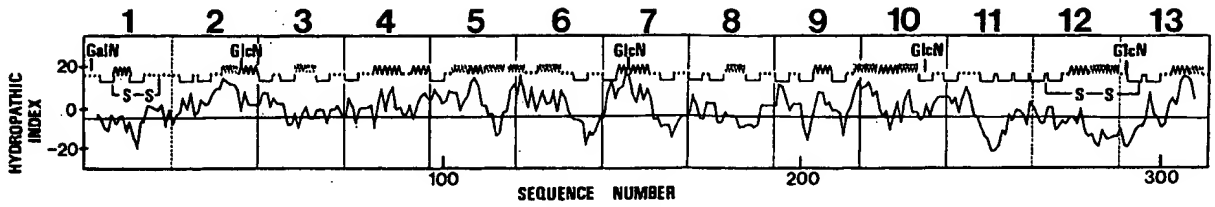

FIG. 4. Hydropathy profile (14) and secondary structure predictions (17) for LRG calculated by use of the PRPLOT program (see text footnote †). In the secondary structure prediction, the residues are represented by dots and are shown in α-helical (⌇⌇⌇), β-sheet (⌇⌇⌇), and β-turn (⌇⌇⌇) conformational states. Locations are given for the oligosaccharides (GalN and GlcN) and for the disulfide bonds. The vertical lines divide the structure into the 13 numbered tandem segments for which the amino acid sequences are given in Fig. 2.

Secondary Structure. The secondary structure predicted by the Chou–Fasman rules (17) shows some repetition of structural elements in the eight tandem conserved segments of the central core of the molecule (shaded section of Fig. 3). In fact, the predicted structure is nearly identical for segments 3 and 8, which have 11 residues in common. Although the predicted secondary structure of the core segments is not identical, the general pattern is similar. Most of the conserved segments begin with a β-turn, followed by an organized structure (either α-helical or β-sheet) in the middle of the segment, and end with a β-turn. The two segments at the amino terminus and the two at the carboxyl terminus are each the loci of a disulfide bond and of carbohydrate, both of which greatly affect the local structure in a way that is hard to predict by the Chou–Fasman rules. These structural characteristics and the homology to mitochondrial proteins and apolipoproteins suggest that LRG is a membrane-derived or membrane-associated protein containing a series of domains capable of bipolar surface orientation.

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SEQ ID NO: 262

RESULT 8
AAV87784
ID AAV87784 standard; cDNA; 686 BP.
XX
AC AAV87784;
XX
DT 12-FEB-1999 (first entry)
XX
DE EST clone ES35.
XX
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO9845437-A2.
XX
PD 15-OCT-1998.
XX
PF 10-APR-1998; 98WO-US06956.
XX
PR 10-APR-1997; 97US-0837312.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1999-070078/06.
XX
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries
XX
PS Claim 1; Page 178; 641pp; English.
XX
CC The present sequence represents an expressed sequence tag (EST), and is
CC a polynucleotide of the invention. The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
CC therapy.
XX
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  Matches 653; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy         129 TTTCTAGAACTCTGTTCCTGCTGCTGCTGTTGGCAGCCTCAGCCTGGGGGGTCACCCTGA 188
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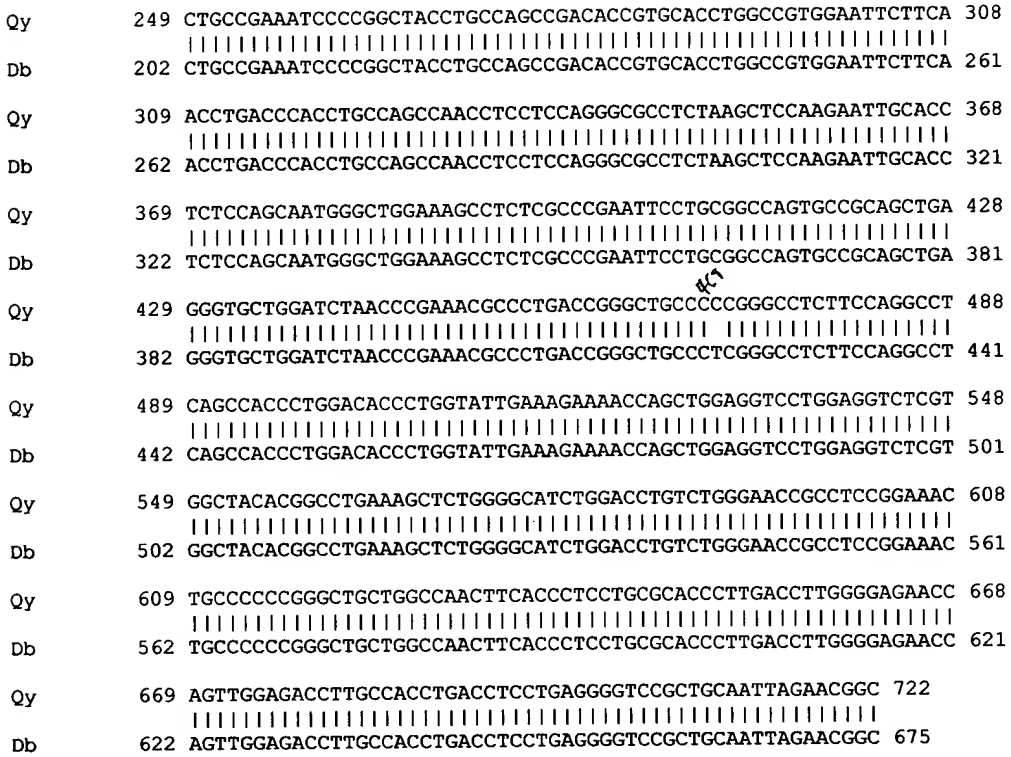
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